

The diagram illustrates the structure of the 11g-5 gene and its expression. The gene structure is shown as a series of exons (white boxes) and introns (lines with arrows). The exons are labeled S, ARR, TM, TK, and TK. The introns are labeled 1, 2, and 3. The gene is flanked by G/E regions. The expression diagram shows the gene being transcribed into mRNA (arrows) and then translated into protein (arrows). A scale bar indicates 0.5 kb.

Figure 1

1	MWSWKCLLFWAVLVTATLCT	TLPEQAQPWGAPVEVESFLVHPGDL	1	RRDDVQSIINWLRDGVQLAE	75									
2	MWSWKCLLFWAVLVTAT	SPTLPEQAQPWGAPVEVESFLVHPGDL		RRDDVQSIINWLRDGVQLAE	75									
3	MWSWKCLLFWAVLVTAT	PSPTLPEC			30									
4	MWSWKCLLFWAVLVTATLCTARPSPTLPEC				30									
5	MWSWKCLLFWAVLVTATLCTARPSPTLPEC				30									
6	MWSWKCLLFWAVLVTATLCTARPSPTLPEC				30									
ARR														
	SNRTRITGEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSS	EDDDDDDDSSSEKETDNTKPN			148									
	SNRTRITGEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSS	EDDDDDDDSSSEKETDNTKPN			150									
		DALPSS	EDDDDDSSSEKETDNTKPN		59									
		DALPSS	EDDDDDSSSEKETDNTKPN		61									
		DALPSS	EDDDDDSSSEKETDNTKPN		59									
		DALPSS	EDDDDDSSSEKETDNTKPN		61									
2														
	VAPYWTSP	EXMEKKLHAPPAKTVKFCPS	SGTNP	TLRWLXNGKEFKPDHRI	GGYKVRATWSIIMDSVVP	SDK	223							
	VAPYWTSP	EXMEKKLHAPPAKTVKFCPS	SGTNP	TLRWLXNGKEFKPDHRI	GGYKVRATWSIIMDSVVP	SDK	225							
	VAPYWTSP	EXMEKKLHAPPAKTVKFCPS	SGTNP	TLRWLXNGKEFKPDHRI	GGYKVRATWSIIMDSVVP	SDK	134							
	VAPYWTSP	EXMEKKLHAPPAKTVKFCPS	SGTNP	TLRWLXNGKEFKPDHRI	GGYKVRATWSIIMDSVVP	SDK	136							
	VAPYWTSP	EXMEKKLHAPPAKTVKFCPS	SGTNP	TLRWLXNGKEFKPDHRI	GGYKVRATWSIIMDSVVP	SDK	134							
	VAPYWTSP	EXMEKKLHAPPAKTVKFCPS	SGTNP	TLRWLXNGKEFKPDHRI	GGYKVRATWSIIMDSVVP	SDK	135							
P2														
	GNVTCIVENEXGS	INHTYQLDVVERS	PHRP	ILQAGLP	ANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKI	298								
	GNVTCIVENEXGS	INHTYQLDVVERS	PHRP	ILQAGLP	ANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKI	300								
	GNVTCIVENEXGS	INHTYQLDVVERS	PHRP	ILQAGLP	ANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKI	209								
	GNVTCIVENEXGS	INHTYQLDVVERS	PHRP	ILQAGLP	ANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKI	211								
	GNVTCIVENEXGS	INHTYQLDVVERS	PHRP	ILQAGLP	ANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKI	209								
	GNVTCIVENEXGS	INHTYQLDVVERS	PHRP	ILQAGLP	ANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKI	211								
P3														
	GPDNL	PYVQILKTAGVNTTD	KEMVLHLRNVS	FEDAGEYTC	LAGNSIGLSHHS	AWLTVLEALEERP	AVMTS	PLYL	373					
	GPDNL	PYVQILKTAGVNTTD	KEMVLHLRNVS	FEDAGEYTC	LAGNSIGLSHHS	AWLTVLEALEERP	AVMTS	PLYL	375					
	GPDNL	PYVQILKTAGVNTTD	KEMVLHLRNVS	FEDAGEYTC	LAGNSIGLSHHS	AWLTVLEALEERP	AVMTS	PLYL	284					
	GPDNL	PYVQILKTAGVNTTD	KEMVLHLRNVS	FEDAGEYTC	LAGNSIGLSHHS	AWLTVLEALEERP	AVMTS	PLYL	286					
	GPDNL	PYVQILK	IMAPV	VGQSTGKETT	VSGAQV	VGR	LSCPR	MGST	TLQAT	HL	SRLATS	PRTS	NRGHKV	284
	GPDNL	PYVQILK	IMAPV	VGQSTGKETT	VSGAQV	VGR	LSCPR	MGST	TLQAT	HL	SRLATS	PRTS	NRGHKV	286
TM														
	IIIIYCTGAFLIS	CMVGSVIVY	KMSG	TKKSD	DFHSCMAVHKLAKS	IP	LRRQVTV	SADSSASMNSGVLLVR	PSRLS	448				
	IIIIYCTGAFLIS	CMVGSVIVY	KMSG	TKKSD	DFHSCMAVHKLAKS	IP	LRRQVTV	SADSSASMNSGVLLVR	PSRLS	450				
	IIIIYCTGAFLIS	CMVGSVIVY	KMSG	TKKSD	DFHSCMAVHKLAKS	IP	LRRQVTV	SADSSASMNSGVLLVR	PSRLS	359				
	IIIIYCTGAFLIS	CMVGSVIVY	KMSG	TKKSD	DFHSCMAVHKLAKS	IP	LRRQVTV	SADSSASMNSGVLLVR	PSRLS	361				
	EVSWEQR	PGMGAGL								300				
	EVSWEQR	PGMGAGL								302				
TK														
	SSGT?	MLAGVSEYEL	PEDPRWEL	PRDLVLGK	PLGEGCF	GQVVLAE	AIGLDK	KPNRVTKVAVKMLKSD	ATEKDL	523				
	SSGT?	MLAGVSEYEL	PEDPRWEL	PRDLVLGK	PLGEGCF	GQVVLAE	AIGLDK	KPNRVTKVAVKMLKSD	ATEKDL	525				
	SSGT?	MLAGVSEYEL	PEDPRWEL	PRDLVLGK	PLGEGCF	GQVVLAE	AIGLDK	KPNRVTKVAVKMLKSD	ATEKDL	434				
	SSGT?	MLAGVSEYEL	PEDPRWEL	PRDLVLGK	PLGEGCF	GQVVLAE	AIGLDK	KPNRVTKVAVKMLKSD	ATEKDL	436				
	SDLISEMEM	KMIGKHKNI	INLLGACTQD	GPLYVIVEY	ASKGNLREYLQARRP	PGLEYCYNP	SHNP	P	EQLSSKDL	598				
	SDLISEMEM	KMIGKHKNI	INLLGACTQD	GPLYVIVEY	ASKGNLREYLQARRP	PGLEYCYNP	SHNP	P	EQLSSKDL	600				
	SDLISEMEM	KMIGKHKNI	INLLGACTQD	GPLYVIVEY	ASKGNLREYLQARRP	PGLEYCYNP	SHNP	P	EQLSSKDL	509				
	SDLISEMEM	KMIGKHKNI	INLLGACTQD	GPLYVIVEY	ASKGNLREYLQARRP	PGLEYCYNP	SHNP	P	EQLSSKDL	511				
	VSCAYQVARGMEYL	ASKKCIHRDLAARNVL	VTEDNVMK	IA	DFGLARDIHHIDY	YKTTNGRLPVK	WMAPEAL	FDR	673					
	VSCAYQVARGMEYL	ASKKCIHRDLAARNVL	VTEDNVMK	IA	DFGLARDIHHIDY	YKTTNGRLPVK	WMAPEAL	FDR	675					
	VSCAYQVARGMEYL	ASKKCIHRDLAARNVL	VTEDNVMK	IA	DFGLARDIHHIDY	YKTTNGRLPVK	WMAPEAL	FDR	584					
	VSCAYQVARGMEYL	ASKKCIHRDLAARNVL	VTEDNVMK	IA	DFGLARDIHHIDY	YKTTNGRLPVK	WMAPEAL	FDR	586					
TK														
	IYTHQSDVWS	FGVLLWEIFTLGGSPYP	GPVVEELFKLLKEGHRMDK?	SNCTNELYMMRDC	WHA	VP	SQRPT	TFKQL	743					
	IYTHQSDVWS	FGVLLWEIFTLGGSPYP	GPVVEELFKLLKEGHRMDK?	SNCTNELYMMRDC	WHA	VP	SQRPT	TFKQL	750					
	IYTHQSDVWS	FGVLLWEIFTLGGSPYP	GPVVEELFKLLKEGHRMDK?	SNCTNELYMMRDC	WHA	VP	SQRPT	TFKQL	659					
	IYTHQSDVWS	FGVLLWEIFTLGGSPYP	GPVVEELFKLLKEGHRMDK?	SNCTNELYMMRDC	WHA	VP	SQRPT	TFKQL	61					
	VEDLDRIVALTS	NOEYLDLSMPLDQYSP	SFPDTRSSTCSSG	DSVFSHEPLPEEP	CLPRHP	AQLANGGLKRR			820					
	VEDLDRIVALTS	NOEYLDLSMPLDQYSP	SFPDTRSSTCSSG	DSVFSHEPLPEEP	CLPRHP	AQLANGGLKRR			822					
	VEDLDRIVALTS	NOEYLDLSMPLDQYSP	SFPDTRSSTCSSG	DSVFSHEPLPEEP	CLPRHP	AQLANGGLKRR			731					
	VEDLDRIVALTS	NOEYLDLSMPLDQYSP	SFPDTRSSTCSSG	DSVFSHEPLPEEP	CLPRHP	AQLANGGLKRR			733					

Figure 2